

## AMENDMENTS TO THE SPECIFICATION

At page 1 before the heading "Background of the Invention," please insert the following heading and paragraph:

## CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of U.S. Application No. 10/604,943, filed August 28, 2003, and this application claims the benefit of U.S. Provisional Application No. 60/441,230, filed January 17, 2003; and U.S. Application No. 10/604,943 is a continuation-in-part of U.S. Application No. 10/604,942, filed August 27, 2003, and U.S. Application No. 10/604,943 claims the benefit of U.S. Provisional Application No. 60/441,241, filed January 17, 2003; and U.S. Application No. 10/604,942 is a continuation-in-part of U.S. Application No. 10/604,945, filed August 27, 2003, which is a continuation of U.S. Application No. 10/303,778, filed November 26, 2002.

Please replace paragraph [0051] with the following replacement paragraph:

FIG. 12A is an annotated sequence of EST72223 (**SEQ ID NO: 415**) comprising novel gene GAM24 (**SEQ ID NO: 419**) detected by the gene detection system of the present invention;

Please replace paragraph [0054] with the following replacement paragraph:

FIG. 13A is an annotated sequence of an EST7929020 (**SEQ ID NO: 416**) comprising novel genes GAM23 (**SEQ ID NO: 420**) and GAM25 (**SEQ ID NO: 421**) detected by the gene detection system of the present invention;

Please replace paragraph [0057] with the following replacement paragraph:

FIG. 14A is an annotated sequence of an EST1388749 (**SEQ ID NO: 417**) comprising novel gene GAM26 (**SEQ ID NO: 422**) detected by the gene detection system of the present invention;

Please replace paragraph [0066] with the following replacement paragraph:

VGAM PRECURSOR RNA folds onto itself, forming VGAM FOLDED PRECURSOR RNA. As FIG. 8 illustrates, VGAM FOLDED PRECURSOR RNA forms a "hairpin structure", folding onto itself. As is well known in the art, this "hairpin structure", is typical genes of the miRNA genes, and is due to the fact that nucleotide sequence of the first half of the RNA of a gene in this group is an accurate or partial inversed-reversed sequence of the nucleotide sequence of its second half. By "inversed-reversed" is meant a sequence which is reversed and

wherein each nucleotide is replaced by a complimentary nucleotide, as is well known in the art (e.g. ATGGC [SEQ ID NO: 407] is the inversed-reversed sequence of GCCAT [SEQ ID NO: 408]).

Please replace paragraph [0146] with the following replacement paragraph:

Reference is now made to FIG. 12A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. FIG. 12A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST72223 (SEQ ID NO: 415). It is appreciated that the sequence of this EST comprises sequences of one known miRNA gene, identified as MIR98 (SEQ ID NO: 418), and of one novel GAM gene, referred to here as GAM24 (SEQ ID NO: 419), detected by the bioinformatic gene detection system of the present invention, described hereinabove with reference to FIG. 2.

Please replace paragraph [0151] with the following replacement paragraph:

*Transcript preparations:* Digoxigenin (DIG) labeled transcripts were prepared from EST72223 (TIGER), MIR98 and predicted precursor hairpins by using a DIG RNA labeling kit (Roche Molecular Biochemicals) according to the manufacture's protocol. Briefly, PCR products with T7 promoter at the 5' end or T3 promoter at the 3' end were prepared from each DNA in order to use it as a template to prepare sense and antisense transcripts, respectively. MIR-98 was amplified using EST72223 as a **template** ~~templet~~ with T7miR98 forward primer: 5'-TAATACGACTCACTATAGGGTGAGGTAGTAAGTTGTATTGTT-3' (SEQ ID NO: 409) and T3miR98 **reverse** ~~revse~~ primer: 5'-AATTAACCCTCAC TAAAGGGAAAGTAGTAAGTTGTATAGTT-3' (SEQ ID NO: 410). EST72223 was amplified with T7-EST 72223 forward primer: 5'-TAATACGAC TCACTATAGGCCCTTATTAGAGGATTCTGCT-3' (SEQ ID NO: 411) and T3-EST72223 reverse primer: 5'-AATTAACCCTCACTAAAGGTTTTTTTTC CTGAGACAGAGT-3' (SEQ ID NO: 412). Bet-4 was amplified using EST72223 as a **template** ~~templet~~ with Bet-4 forward primer: 5'-GAGGCAGGA GAATTGCTTGA-3' (SEQ ID NO: 413) and T3-EST72223 reverse primer: 5'-AATTAACCCTCACTAAAGGCCTGAGACAGAGTCTTGCTC-3' (SEQ ID NO: 414). The PCR products were cleaned and used for DIG-labeled or unlabeled transcription reactions with the appropriate polymerase. For transfection experiments, CAP reaction was performed by using a mMessage mMachine kit (Ambion).

Please replace paragraph [0157] with the following replacement paragraph:

Reference is now made to FIG. 13A which is an annotated sequence of an EST comprising a novel gene detected by the gene detection system of the present invention. FIG. 13A shows the nucleotide sequence of a known human non-protein coding EST (Expressed Sequence Tag), identified as EST 7929020 (SEQ

Please replace paragraph [0160] with the following replacement paragraph:

Please replace Table 2 with the following replacement Table 2:

GENE	G-SEQID	TARGET	UTR	SEQUENCE	T-SEQID	BINDING-SITE
GAM15	<u>423</u>	PRIM2A	3'	CAGGCAGATCTCAGACTC	50	<div> <div>C</div> <div>TCAGA</div> <div>GAGTC GAGATCT CCTG</div> <div>               </div> <div>CTCAG CTCTAGA GGAC</div> <div>A C</div> </div>
GAM15	<u>424</u>	RAP1B	3'	CCAGGTCTGAAGAACTGTTGCC CA	142	<div> <div>A CCG A</div> <div>TG GT AG TCTTCAGACCTGG</div> <div>              </div> <div>AC CG TC AGAAGTCTGGACC</div> <div>C TTG A</div> </div>
GAM15	<u>424</u>	RET	3'	CCAGGTCTAAACAGCTGACCCA	173	<div> <div>A CG ATCTTC</div> <div>TG GTC AG AGACCTGG</div> <div>               </div> <div>AC CAG TC TCTGGACC</div> <div>C GACAAA</div> </div>
GAM15	<u>424</u>	RET	3'	CCAGGTCTAAACAGCTGACCCA	174	<div> <div>A CG ATCTTC</div> <div>TG GTC AG AGACCTGG</div> <div>               </div> <div>AC CAG TC TCTGGACC</div> <div>C GACAAA</div> </div>
GAM15	<u>424</u>	RET	3'	CCAGGTCTAAACAGCTGACCCA	179	<div> <div>A CG ATCTTC</div> <div>TG GTC AG AGACCTGG</div> <div>               </div> <div>AC CAG TC TCTGGACC</div> <div>C GACAAA</div> </div>
GAM15	<u>424</u>	RET	3'	CCAGGTCTAAACAGCTGACCCA	37	<div> <div>A CG ATCTTC</div> <div>TG GTC AG AGACCTGG</div> <div>               </div> <div>AC CAG TC TCTGGACC</div> <div>C GACAAA</div> </div>
GAM15	<u>425</u>	AMOTL1	3'	CTGATAAAGATTTCAGACTCA	304	<div> <div>C</div> <div>GACAAA</div> <div>TGAGTC GAGATCT TCAG</div> <div>               </div> <div>ACTCAG CTTTAGA AGTC</div> <div>A AAT</div> </div>
GAM15	<u>424</u>	DGKZ	3'	CCAGACCTAGGGCTGGACTCA	70	<div> <div>A G A C AC</div> <div>TGAGTCC AG TCTT AG CTGG</div> <div>                </div> <div>ACTCAGG TC GGGA TC GACC</div> </div>

GAM15 426 DKFZP586G1122 3' CAGGTCTAGCCGGGCCCA 265

GAM15 424 FLJ22127 3' CCAGGCCTGAATGGATGGACTC 192  
A

GAM15 423 LOC126248 3' CAGCCCTGGCTGGACTC 308

GAM15 424 LOC146640 5' CCAGGTGACCTACCCGGACTCA 323

GAM15 424 LOC153416 3' CCAGGTCTGAAGAACTGTTGCC 263  
CA

GAM15 424 LOC220790 3' CCAGGTCTGAAGAACTGTTGCC 378  
CA

GAM16 427 PRKG2 3' CATGGTGGTATCTTAAAA 103

GAM16 427 AFAP 3' CATAGCAGGGCGTCTGTAAAA 183

GAM16 427 C3AR1 3' CATAGTGAAAGTTTATAAGA 76

GAM16 427 FLJ22029 3' CATGAAAATGTCTATAGAA 203

GAM16 427 SEMA5A 3' CATAGTGACGTCCTGAAGA 72

GAM16 427 UNC5D 3' CATAGGATTTCTATAGAA 234

GAM16 428 LOC129446 3' CATAGAATGTGTCTATAAA 315

GAM16 427 LOC153396 3' CATAGTGGCTGCCTATAGAA 338

CA  
A AGAT TC  
TG GTCCG CT AGACCTG  
|| ||||| || |||||  
AC CGGC GA TCTGGAC  
C C A  
GAG A  
TGAGTCC ATCT TCAG CCTGG  
|| ||||| || |||||  
ACTCAGG TAGG AGTC GGACC  
TA C  
G ATCT AC  
GAGTCC AG TCAG CT G  
|| ||||| || |||||  
CTCAGG TC GGTC GA C  
CC A  
AGATCT AG  
TGAGTCCG TC ACCTGG  
|| ||||| || |||||  
ACTCAGGC AG TGGACC  
CCATCC  
A CCG A  
TG GT AG TCTTCAGACCTGG  
|| || || |||||  
AC CG TC AGAAGTCTGGACC  
C TTG A  
A CCG A  
TG GT AG TCTTCAGACCTGG  
|| || || |||||  
AC CG TC AGAAGTCTGGACC  
C TTG A  
T C  
TTTTA AGA ATCACTATG  
|| || || |||||  
AAAAT TCT TGGTGGTAC  
A  
A A  
TTTTATAGAC TC CTATG  
|| ||||| || |||||  
AAAATGTCTG GG GATAC  
CG AC  
A  
TTTTATAGAC TCACTATG  
|| ||||| || |||||  
AGAATATTG AGTGATAC  
AA  
CAC  
TTTTATAGACAT TATG  
|| ||||| || |||||  
AAGATATCTGTA GTAC  
AAA  
ATA A  
TTTT GAC TCACTATG  
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AGAA CTG AGTGATAC  
GTC C  
C A  
TTTTATAGA ATC CTATG  
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AAGATATCT TAG GATAC  
T  
CA  
TTTTATAGACAT CTATG  
|| ||||| || |||||  
AAATATCTGTG GATAC  
TAA  
A  
TTTTATAG CA TCACTATG  
|| ||||| || |||||  
AAGATATC GT GGTGATAC  
C C

GAM16 427 LOC50999 3' CATAATGGTGTCTTAAAA 145

GAM17 429 KIAA0830 3' AACATTATGCTTACTGCATC 290

GAM17 430 PREI3 3' AACATTATGTACTGTATATATC 275  
AT

GAM17 431 SEC15L 3' ACATATGCCTCTACTCATA 297

GAM17 432 LOC152317 3' AACATCAATGGACTCTGTATCA 352

GAM18 433 DSCR1 3' CATTTTGAAATACTTAA 81

GAM18 434 ELMO2 3' CCAGGAGAAACACTTA 235

GAM18 434 ELMO2 3' CCAGGAGAAACACTTA 186

GAM18 435 FGF5 3' CCACAGGGAGCAAACACTTAG 227

GAM18 435 FGF5 3' CCACAGGGAGCAAACACTTAG 83

GAM18 435 NEFH 3' CCACACGTAAACACTTGA 180

GAM18 435 NFIB 3' CCACAAAAGAAACACTTAA 93

GAM18 435 PRKY 3' CCATAAATGAAACACTTGA 62

GAM18 434 RNF18 5' CCACAATTGGGTTCTTA 172

GAM18 435 SLC1A3 3' CCACAATTGAAATTTTAA 77

T C  
TTTTA AGACATCA TATG  
||||| ||||||||| |||||  
AAAAT TCTGTGGT ATAC  
A  
A TA  
GAT CAG AGG CATAATGTT  
||| ||| ||| |||||||||  
CTA GTC TTC GTATTACAA  
C A  
CAGA  
ATGATA GGTACATAATGTT  
||||| |||||||||||||  
TACTAT TCATGTATTACAA  
ATATG  
TAC CATA  
TATGA AGAGGTA ATGT  
||||| ||||||||| |||||  
ATACT TCTCCGT TACA  
CA A  
GTA A  
TGATACAGAG CAT ATGTT  
||||||||||| ||| |||||  
ACTATGTCTC GTA TACAA  
AG AC  
TT  
TTAAGTGTTC CAA GTG  
||||||||||||| |||  
AATTCATAAAGTT TAC  
T  
AA G  
TAAGTGTTC TT TGG  
||||||||||| || |||  
ATTCACAAAG AG ACC  
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AA G  
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CAA  
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CAA  
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CGAGG  
CAAT  
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TGC  
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AA  
A  
TTAAGTGTTC TTGTGG  
||||||||||| |||||||  
AGTTCACAAAGT AATACC  
A  
TGT  
TAAG TTCAATTGTGG  
||| |||||||||||  
ATTC GGGTTAACACC  
TT  
T

						TTAAG GTTTC AATTGTGG                         AATTT TAAAGTTAACACC T AATT TTAAGTGTTC GTGG                         AATTACAAAG TACC
GAM18	<u>435</u>	VMD2	3'	CCATTGGAAACATTTAA	78	GT AAT G TTAAGTGTTC T TGG                         AATTCACAGAG G ACC
GAM18	<u>435</u>	XRCC3	5'	CCAGGGAGACACTTAA	91	G AT TTAAGTGTTC TGTGG                         AATTACAAAGT ATATC
GAM18	<u>435</u>	ARHGAP5	3'	CTATATGAAACATTTAA	321	ATT TTAAGTGTTC GTGG                         AATTCACAAAGT TACC
GAM18	<u>435</u>	EFA6R	3'	CCATTGTGAAACACTTAA	140	GT T AT TTAAGTGTTC CA TGTGG                         AATTCACAA GT ACACC
GAM18	<u>434</u>	KIAA0903	3'	CCACATGTAACACTTA	294	T GTGTTT CAATTGTGG                         TACAAG GTTACACC
GAM18	<u>436</u>	KIAA1244	3'	CCACAATTGTCTGAACAT	295	TCT CA TG TTAAGTGTTC AT TGG                         AATTCACAAG TG GTC
GAM18	<u>435</u>	Rpo1-2	3'	CTGTGGTAAGAACACTTAA	214	AA GT AA TTAAGTGTTC TTGTGG                         AGTTCACAAAG AACACC
GAM18	<u>435</u>	LOC115574	3'	CCACAACCTGGAAACACTTGA	303	GTC TGT TAAG TTCAATTGTGG                         ATTC GGGTTAACACC
GAM18	<u>434</u>	LOC144144	5'	CCACAATTGGGTTCTTA	260	TT AA TTAAGTGTTC TTG TGG                         AATTCACAAAG AAC ACC
GAM18	<u>435</u>	LOC148254	3'	CCATCAAAAGAAACACTTAA	329	AA T ATT TTAAGTGTTC GTGG                         AATTACAAAGT CACC
GAM18	<u>435</u>	LOC157624	5'	CCACTGAAACATTTAA	359	TGT TAAG TTCAATTGTGG                         ATTC GGGTTAACACC
GAM18	<u>434</u>	LOC220486	5'	CCACAATTGGGTTCTTA	374	TT AA A CAG GAAAAAAT AAAGCAT                       GTC CTTTTTTA TTTCGTA
GAM19	<u>437</u>	AGL	3'	ATGCTTTCATTTTTTCACTG	31	A AA C CAG GAAAAAAT AAAGCAT 
GAM19	<u>437</u>	AGL	3'	ATGCTTTCATTTTTTCACTG	43	AA A CAG GAAAAAAT AAAGCAT

[illegible]

[illegible]



GAM19	<u>447</u>	LOC200107 3'	ATGCTTTTACTTTTTCTTTT	364	TC C CC A AGAAGAAAA TAAAGCAT       TTTTCTTTT ATTTTCGTA C
GAM19	<u>448</u>	LOC203340 3'	TGCTTTTATTTTCCTTC	368	AA GAAG AAAATAAAAGCA      CTTC TTTATTTTCGT C
GAM19	<u>443</u>	LOC221271 3'	TGCCTTTTCTGTCA	380	ATAAAA TGACAGAAGAAAA GCA       ACTGCTTTTTTTT CGT C
GAM19	<u>442</u>	LOC254778 3'	ATGCTTTTCTCTATCA	400	C AAATAAA TGA AGAAGAA AGCAT     ACT TCTCTTT TCGTA C
GAM19	<u>449</u>	LOC51312 5'	GCTTTTATTTCTCCTCT	164	A A AGA GA AAAATAAAAGC     TCT CT TTTTATTTTCG C C
GAM19	<u>450</u>	LOC91286 5'	TTTTTATTTCTTTTCTGTCA	273	A TGACAGAAGAA AAATAAAG       ACTGCTTTTT TTTATTTT C
GAM19	<u>451</u>	LOC92223 3'	ATGCTTTTATTGTACCTTC	286	AAAA GAAG AATAAAAGCAT      CTTC TTATTTTCGTA CATG
GAM19	<u>452</u>	LOC92482 5'	TGCATCTTTCTCTGT	288	A AAAA ACAGAAGAAAA AT GCA       TGCTTTCTTT TA CGT C
GAM20	<u>453</u>	ATRN 3'	CTATCTGATGCACAGAA	248	G AAG TT TGTGCATCA GATAG    AA ACACGTAGT CTATC G
GAM20	<u>453</u>	ATRN 3'	CTATCTGATGCACAGAA	248	G AAG TT TGTGCATCA GATAG    AA ACACGTAGT CTATC G
GAM20	<u>454</u>	DKFZP564O0463 3'	CTTTTCTTAATGCATACAATA	127	CAA T TATTGTGTGCAT AGGA AGAG       ATAACATACGTA TTCT TTTC A T
GAM20	<u>454</u>	DKFZP564O0463 3'	CTTTTCTTAATGCATACAATA	127	CAA T TATTGTGTGCAT AGGA AGAG       ATAACATACGTA TTCT TTTC A T
GAM20	<u>454</u>	FLJ13102 3'	CTCTACCCTCTCCACACACA GTA	202	A T CATCAA A TATTGTGTG AGG TAGAG       ATGACACAC TCC ATCTC CACCCTC C CATCAA A
GAM20	<u>454</u>	FLJ13102 3'	CTCTACCCTCTCCACACACA GTA	202	A T TATTGTGTG AGG TAGAG       ATGACACAC TCC ATCTC CACCCTC C CATCAA A

GAM20 453 HSPC014 3' CTGTAATTTGATGTACACAA 144

GAM20 454 HSPC014 3' CTGTAATTTGATGTACACAA 144

GAM20 455 KIAA0040 3' TCTATCCCCTTGTCACATA 129

GAM20 455 KIAA0040 3' TCTATCCCCTTGTCACATA 129

GAM20 456 KIAA0470 3' CCACTTGATGCACAAATA 134

GAM20 456 KIAA0470 3' CCACTTGATGCACAAATA 134

GAM20 457 KIAA1908 5' CTCTCGGGCGATGCACACAA 302

GAM20 457 KIAA1908 5' CTCTCGGGCGATGCACACAA 302

GAM20 454 MGC22014 3' CTCTATCCTTGTATATCACAAAT 269  
A

GAM20 454 MGC22014 3' CTCTATCCTTGTATATCACAAAT 269  
A

GAM20 453 TNRC9 3' CTGTATTTTGTATGCAACAA 293

GAM20 453 TNRC9 3' CTGTATTTTGTATGCAACAA 293

GAM20 454 LOC116123 3' CTTTGGTTTGTATGCATACAATA 243

GAM20 454 LOC116123 3' CTTTGGTTTGTATGCATACAATA 243

GAM20 458 LOC149721 3' CTATCATGTGGATGCACACA 334

GG  
TTGTGTGCATCAAA ATAG  
|||||  
AACACATGTAGTTT TGTC  
AA  
GG  
TTGTGTGCATCAAA ATAG  
|||||  
AACACATGTAGTTT TGTC  
AA  
TCAAA  
TGTGTG CA GGATAGA  
||||| |||  
ATACAC GT CCTATCT  
T TCC  
TCAAA  
TGTGTG CA GGATAGA  
||||| |||  
ATACAC GT CCTATCT  
T TCC  
G A  
TATT TGTGCATCAA GG  
|||||  
ATAA ACACGTAGTT CC  
CA  
G A  
TATT TGTGCATCAA GG  
|||||  
ATAA ACACGTAGTT CC  
CA  
AAAGGAT  
TTGTGTGCATC AGAG  
|||||  
AACACACGTAG TCTC  
CGGGC  
AAAGGAT  
TTGTGTGCATC AGAG  
|||||  
AACACACGTAG TCTC  
CGGGC  
TGCATCA  
TATTGTG AAGGATAGAG  
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ATAACAC TTCCTATCTC  
TATATG  
TGCATCA  
TATTGTG AAGGATAGAG  
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TATATG  
G G  
TTGT TGCATCAAAG ATAG  
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AACA ACGTAGTTTT TGTC  
A  
G  
TTGT TGCATCAAAG ATAG  
|||||  
AACA ACGTAGTTTT TGTC  
A  
GGA  
TATTGTGTGCATCAAA TAGAG  
|||||  
ATAACATACGTAGTTT GTTTC  
G  
GGA  
TATTGTGTGCATCAAA TAGAG  
|||||  
ATAACATACGTAGTTT GTTTC  
G  
AAAG

GAM20 458 LOC149721 3' CTATCATGTGGATGCACACA 334

GAM20 454 LOC153338 5' CTCTATCCCTCTGTGGCCAATA 354

GAM20 454 LOC153338 5' CTCTATCCCTCTGTGGCCAATA 354

GAM20 456 LOC220766 3' CCACTTGATGCACAAATA 375

GAM20 456 LOC220766 3' CCACTTGATGCACAAATA 375

GAM20 453 LOC253351 5' CTGGCACCTGATGCACACAA 402

GAM20 453 LOC253351 5' CTGGCACCTGATGCACACAA 402

GAM20 454 LOC257484 3' CTCTATCCTTGTATATCACAAAT 366  
A

GAM20 454 LOC257484 3' CTCTATCCTTGTATATCACAAAT 366  
A

GAM21 459 KIAA1843 3' ATAGAAAGTAGCCAAAAA 267

GAM21 460 SDFR1 3' AAAGTACAGCAAAACCTA 117

GAM21 460 SDFR1 3' AAAGTACAGCAAAACCTA 150

GAM21 461 LOC132617 3' CTACAGACCATAGCAAAAAC 314

GAM21 461 LOC145622 3' CTATAGAACAAATGCAAAAAC 322

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TGTGTGCATC   GATAG
|||||
ACACACGTAG   CTATC

      GTGTA
      AAAG_
TGTGTGCATC   GATAG
|||||
ACACACGTAG   CTATC

      GTGTA
      T G CAAA
TATTG GT CAT   GGATAGAG
||||| ||| |||
ATAAC CG GTG   CCTATCTC

      TCTC
      T G CAAA
TATTG GT CAT   GGATAGAG
||||| ||| |||
ATAAC CG GTG   CCTATCTC

      TCTC
      G _ _ A_
TATT TGTGCATCAA GG
||||| ||| |||
ATAA ACACGTAGTT CC

      CA
      G _ A_
TATT TGTGCATCAA GG
||||| ||| |||
ATAA ACACGTAGTT CC

      CA
      _ AAGGA
TTGTGTGCATCA TAG
||||| |||
AACACACGTAGT GTC

      CCACG
      AAGGA
TTGTGTGCATCA TAG
||||| |||
AACACACGTAGT GTC

      CCACG
      TGCATCA
TATTGTG AAGGATAGAG
||||| |||
ATAACAC TTCCTATCTC

      TATATG_
      TGCATCA
TATTGTG AAGGATAGAG
||||| |||
ATAACAC TTCCTATCTC

      TATATG_
      CTG
TTTTTG TACTTTCTAT
||||| |||
AAAAAC ATGAAAGATA

      CG_
      T
TAG TTTTGCTGTACTTT
||| |||
ATC AAAACGACATGAAA

      C
      T
TAG TTTTGCTGTACTTT
||| |||
ATC AAAACGACATGAAA

      C
      ACTT A
GTTTTTGCTGT TCT TAG
||||| |||
CAAAAACGATA AGA ATC

      CC_ C
      TGTACT
GTTTTTGC TTCTATAG

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GAM21 462 LOC222681 3' CTACAGAACATGGAGCAAAAAC 386  
TA

GAM21 462 LOC257507 3' CTACAGAACATGGAGCAAAAAC 405  
TA

GAM21 462 LOC257625 3' CTACAGAACATGGAGCAAAAAC 406  
TA

GAM22 463 BTEB1 3' ACCACTACATCCATCT 53

GAM22 464 CEP2 3' ACCACCTCCTTCATCTT 112

GAM22 463 ECM1 3' ACCCTGCCCCACCCATCT 82

GAM22 465 ENG 3' ACCACTTGCCACGCTGTT 34

GAM22 463 ESRRG 3' ACCACTTTTCAGCCATTT 276

GAM22 466 HDAC4 3' ACCACTCGACTCATCTTG 98

GAM22 466 IL6 3' ACCACTTGAAACATTTTA 41

GAM22 466 LRAT 3' ACCACTTAAATTTATCTTA 259

GAM22 466 MYLK2 3' ACCACTCGGGGCCCCCATCTTG 226

GAM22 463 PRKACB 3' ACCACTTCTTTTCATCT 61

GAM22 463 PRLR 3' ACCACTTGCCTCTTTCT 51

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|||||
CAAAAACG
      TAAC
      G CT A
TAGTTTTTGCT TA TTCT TAG
|||||
ATCAAAAACGA GT AAGA ATC
      G AC C
      G CT A
TAGTTTTTGCT TA TTCT TAG
|||||
ATCAAAAACGA GT AAGA ATC
      G AC C
      G CT A
TAGTTTTTGCT TA TTCT TAG
|||||
ATCAAAAACGA GT AAGA ATC
      G AC C
      G AC C
      GCA
AGATGGGTG AGTGGT
|||||
TCTACCTAC TCACCA
      A
      T CAA
AAGATGGG GG GTGGT
|||||
TTCTACTT CC CACCA
      TC
      CA T
AGATGGGTGG AG GGT
|||||
TCTACCCACC TC CCA
      CCG
      GATGG GTGGCAAGTGGT
|||||
TTGTC CACCGTTCACCA
      G
      G C
AGATGG TGG AAGTGGT
|||||
TTTACC ACT TTCACCA
      G T
      G GCA
TAAGATGGGT AGTGGT
|||||
GTTCTACTCA TCACCA
      GC
      GGTGG
TAAGATG CAAGTGGT
|||||
ATTTTAC GTTCACCA
      AAA
      GTGGC
TAAGATGG AAGTGGT
|||||
ATTCTATT TTCACCA
      AAAA
      T A
TAAGATGGG GGC AGTGGT
|||||
GTTCTACCC CCG TCACCA
      GGGC
      T C
AGATGGG GG AAGTGGT
|||||
TCTACTT TC TTCACCA
      T
      T
AGA GGG GGCAAGTGGT
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GAM22	<u>464</u>	SLC6A6	3'	ACCACTTGAATTGATCTT	65	TCT TCT CCGTTCACCA T G - GG AAGAT GGT CAAGTGGT                 TTCTA TTA GTTCACCA G A GGG
GAM22	<u>466</u>	WASF3	3'	ACCACTTGGTCAGAATTTTA	109	TAAGAT TGGC AAGTGGT                 ATTTTA ACTG TTCACCA AG G TG G
GAM22	<u>466</u>	XX	3'	ACCACTTGCACATTTCTTA	181	TAAGA GGTG CAAGTGGT                 ATTCT TCAC GTTCACCA TA A T A
GAM22	<u>463</u>	ZYX	3'	ACCACCTGCCCCACCT	69	AG TGGG GGCA GTGGT                  TC ACCC CCGT CACCA C C
GAM22	<u>463</u>	ARHF	3'	ACCCTGGACCACCCATCT	167	AGATGGGTGG AG GGT                 TCTACCCACC TC CCA AGG CAA
GAM22	<u>467</u>	DDR1	5'	CGCACCACCCATTTTA	57	TAAGATGGGTGG GTG                 ATTTTACCCACC CGC A CAA
GAM22	<u>467</u>	DDR1	5'	CGCACCACCCATTTTA	122	TAAGATGGGTGG GTG                 ATTTTACCCACC CGC A CAA
GAM22	<u>467</u>	DDR1	5'	CGCACCACCCATTTTA	123	TAAGATGGGTGG GTG                 ATTTTACCCACC CGC A CAA
GAM22	<u>466</u>	DKFZP547E1010	5'	ACCACCTCCCTATCTTA	141	TAAGATGGG G GTGGT                 ATTCTATCC C CACCA CT TG CAA
GAM22	<u>466</u>	DKFZP547E1010	5'	ACCACCTCCCTATCTTA	280	TAAGATGGG G GTGGT                 ATTCTATCC C CACCA CT TG CAA
GAM22	<u>463</u>	FLJ11715	3'	ACCGCGCCAGCCCATCT	197	AGATGGGT GGC GTGGT                 TCTACCCG CCG CGCCA AC AAG
GAM22	<u>463</u>	FLJ12587	3'	ACCAGGCGCATCCATCT	190	AGATGG GTGGC TGGT                 TCTACC CGCCG ACCA TA GG
GAM22	<u>465</u>	FLJ12650	3'	ACCACTTGCCAATGCCTCTC	196	GA GGT GGCAAGTGGT              CT TCCG CCGTTCACCA C TAA
GAM22	<u>468</u>	FLJ13265	3'	ACCACTTGCCCTGCCTCA	201	TG GGT GGCAAGTGGT              AC CCG CCGTTCACCA

GAM22 463 FLJ20546 3' ACCTCTGCCACCCATCT 155

GAM22 466 FLJ32865 3' ACCACCACGCCCAGCTTA 251

GAM22 463 GPR88 3' ACCACTTGTTGTACATCT 185

GAM22 463 HSPC216 3' ACCTGACCACCCATTT 149

GAM22 466 JIK 3' ACCACATTCCCCATTTTA 148

GAM22 466 KIAA0153 3' ACCACCCAGCAAGCCCGCCTTA 139

GAM22 466 KIAA0215 3' ACCAGGAGACCACCATCTTA 130

GAM22 468 KIAA0461 3' ACCACTTGTTGAAATCCA 291

GAM22 466 MEGF10 3' ACCACAGACTCATCTTA 216

GAM22 468 MGC2452 5' ACCACTAATTGCCACTCA 218

GAM22 466 MGC4796 3' ACCTTCACCTCATCTTA 266

GAM22 463 MRPL10 3' ACCACATGTACCCATTT 256

GAM22 466 MRPL42 5' ACCACTTGATAAGCATCTTG 299

GAM22 464 POLYDOM 3' ACCACTGCTATCCATCTT 195

T TC A T  
AGATGGGTGGCA G GGT  
|||||  
TCTACCCACCGT C CCA

A GCAA T  
TAAG TGGGTG GTGGT  
|||||  
ATTG ACCCGC CACCA

G AC  
G TG  
AGATG G GCAAGTGGT  
|||||  
TCTAC T TGTTACCA

A GT  
AGT  
AGATGGGTGG CA GGT  
|||||  
TTTACCCACC GT CCA

A  
T CAA  
TAAGATGGG GG GTGGT  
|||||  
ATTTTACCC CT CACCA

A G AA  
TAAG TGGGT GC GTGGT  
|||||  
ATTG GCCCG CG CACCA

C AA ACC  
G CAAG  
TAAGATGG TGG TGGT  
|||||  
ATTCTACC ACC ACCA

AGAGG  
TGGGT GGCAAGTGGT  
|||||  
ACCTA TTGTTACCA

AAG  
GGCAA  
TAAGATGGGT GTGGT  
|||||  
ATTCTACTCA CACCA

GA  
TGGGTGGCA AGTGGT  
|||||  
ACTCACCGT TCACCA

TAA CAAGT  
TAAGATG GGTGG GGT  
|||||  
ATTCTAC CCACT CCA

T T  
G  
AGATGGGTG CAA GTGGT  
|||||  
TTTACCCAT GTT CACCA

A  
GG G  
TAAGATG TG CAAGTGGT  
|||||  
GTTCTAC AT GTTCACCA

GA A  
A  
AAGATGGGTGGCA GTGGT  
|||||  
TTCTACCTATCGT CACCA

GAM22	<u>463</u>	PRO0246	5'	ACCACTTGCTATGGTCT	126	GG AGAT GTGGCAAGTGGT             TCTG TATCGTTCACCA
GAM22	<u>466</u>	SMCR7	3'	ATGACTTGCCACCCACCT	247	G_ A G AG TGGGTGGCAAGT GT          TC ACCCACC GTTCA TA
GAM22	<u>466</u>	TPD52	3'	ACCACTTATATCAACTTA	88	C G ATG GC TAAG GGTG AAGTGGT             ATTC CTAT TTCACCA
GAM22	<u>464</u>	ZNF384	3'	ACCACTCATCACGCCATCTT	239	AA_ A_ CA AAGATGG GTGG AGTGGT             TTCTACC CACT TCACCA
GAM22	<u>466</u>	LOC124216	3'	ACCTCTCCTCACCACATCTTA	307	GG AC CA T TAAGATGGGTGG AG GGT             ATTCTACCCACT TC CCA
GAM22	<u>463</u>	LOC144509	5'	ACCACCAGCTGCACCCATCT	320	CC T AA AGATGGGTG GC GTGGT             TCTACCCAC CG CACCA
GAM22	<u>463</u>	LOC146822	3'	ACCACCTGCCCTACCATT	324	GT AC A AGATGG GGCA GTGGT             TTTACC CCGT CACCA
GAM22	<u>463</u>	LOC148371	5'	ACCACTTCTGGCCATCT	330	ATC C G C AGATGG TGG AAGTGGT             TCTACC GTC TTCACCA
GAM22	<u>464</u>	LOC149373	3'	ACCTGCCGGCCACCCATTCA	333	G - AA A GATGGGTGGC GT GGT         A TTACCCACCG CG CCA
GAM22	<u>466</u>	LOC151146	5'	ACCCCCAGCCCATCTTA	336	C GC T CAAGT TAAGATGGG TGG GGT             ATTCTACCC ACC CCA
GAM22	<u>466</u>	LOC157562	5'	ACCACCCAGTCATTTTA	357	G CC G CAA TAAGATGG TGG GTGGT             ATTTTACT ACC CACCA
GAM22	<u>466</u>	LOC160897	3'	ACCACTTATAATGCCTCATCTT	341	G GC A TAAGATG GGTG AAGTGGT             ATTCTAC CCGT TTCACCA
GAM22	<u>463</u>	LOC161589	5'	ACCACTGCTGGCCATCT	343	T AATA G A AGATGG TGGCA GTGGT             TCTACC GTCGT CACCA
GAM22	<u>468</u>	LOC163682	5'	ACCACTTGCCGAGCTCCTA	361	G - TGGG TGGCAAGTGGT             ATCC GCCGTTACCA
GAM22	<u>466</u>	LOC199692	3'	ACCAGTAACCTATCTTA	257	TCGA G AAG

GAM22	<u>463</u>	LOC202108	5'	ACCACTACTGGCCATCT	367
GAM22	<u>464</u>	LOC221468	3'	ACCACCCAGTTCTTCATCTT	258
GAM22	<u>463</u>	LOC221838	5'	ACCACTACTGGCCATCT	385
GAM22	<u>463</u>	LOC221839	5'	ACCACTACTGGCCATCT	384
GAM22	<u>465</u>	LOC90313	5'	ACCACCCCTGTGCCCATC	268
GAM22	<u>466</u>	LOC92399	3'	ACCACCTGCTCCTCATCTTA	242
GAM23	<u>469</u>	ADAM8	3'	AGAGAAGCCATGCGTTCC	52
GAM23	<u>469</u>	BN51T	3'	AGAGAGCAAGGATTGAGTCTG	363
GAM23	<u>469</u>	CD3Z	3'	AGACTGACCTTGATGAGCTG	48
GAM23	<u>470</u>	DAAM2	3'	AGGTGCTTGATGAATCTG	381
GAM23	<u>471</u>	DLG4	3'	AGGGAGGGATGGGTCT	54
GAM23	<u>472</u>	DMD	5'	AGAAAAGCTTGAGCAAGTC	73
GAM23	<u>472</u>	DMD	5'	AGAAAAGCTTGAGCAAGTC	74
GAM23	<u>472</u>	DMD	5'	AGAAAAGCTTGAGCAAGTC	75

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TAAGATGGGT GC   TGGT
||||| |||
ATTCTATCCA TG   ACCA
      A
      G   CA
AGATGG TGG AGTGGT
||||| |||
TCTACC GTC TCACCA
      G   A
      TG   AA
AAGATGGG GC   GTGGT
||||| |||
TTCTACTT TG   CACCA
      CT   ACC
      G   CA
AGATGG TGG AGTGGT
||||| |||
TCTACC GTC TCACCA
      G   A
      G   CA
AGATGG TGG AGTGGT
||||| |||
TCTACC GTC TCACCA
      G   A
      G   A
GATGGGTG CA   GTGGT
||||| |||
CTACCCGT GT   CACCA
      CCC
      TG   A
TAAGATGGG GCA GTGGT
||||| |||
ATTCTACTC CGT CACCA
      CT   C
      A   T   CAA
C GAC CAT GCTTCTCT
| ||| |||
C TTG GTA CGAAGAGA
      C   C   C
      AA   T
CAGACTCA TC   GCT CTCT
||||| |||
GTCTGAGT AG   CGA GAGA
      T   GAA
      A   C   C
CAG CTCATCAAG TT TCT
||| |||
GTC GAGTAGTTC AG AGA
      C   TC
      C   T
CAGA TCATCAAG TCT
||| |||
GTCT AGTAGTTCG GGA
      A   T
      AAG
AGACTCATC CTTCTCT
||||| |||
TCTGGGTAG GGAGGGA
      CA   C
GACT TCAAGCTT TCT
||| |||
CTGA AGTTCGAA AGA
      ACG   A
      CA   C
GACT TCAAGCTT TCT
||| |||
CTGA AGTTCGAA AGA
      ACG   A
      CA   C
GACT TCAAGCTT TCT

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CTGA AGTTCGAA AGA  
ACG A  
A  
CAG CTCATCAA GCTT  
||||| |||||  
GTC GAGTGGTT CGGA  
C TCTC  
CA AA  
AGACT TC GCTTCTCT  
||||| |||||  
TCTGG AG CGAAGAGA  
GAC  
A AA  
GA CTC TC GCTTCTCT  
||||| |||||  
CT GAG GG CGAAGAGA  
C GA  
A A T  
C GACTCATCA GC TCT  
||||| |||||  
A TTGAGTAGT CG GGA  
C C C  
A A T  
C GACTCATCA GC TCT  
||||| |||||  
A TTGAGTAGT CG GGA  
C C C  
A A T  
C GACTCATCA GC TCT  
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A TTGAGTAGT CG GGA  
C C C  
A A T  
C GACTCATCA GC TCT  
||||| |||||  
A TTGAGTAGT CG GGA  
C C C  
A CA A  
CAG CT TC AGCTTCTCT  
||||| |||||  
GTC GA AG TCGAAGAGA  
C G  
A CA A  
CAG CT TC AGCTTCTCT  
||||| |||||  
GTC GA AG TCGAAGAGA  
C G  
CT A  
GA CATCA GCTTCTCT  
|| |  
CT GTAGT CGAAGAGA  
CC CAAGC  
CAGACTCAT TTCTCT  
||||| |||||  
GTTTGAGTG AAGAGA  
AGCA  
CTC A  
CAGA ATCA GCTTCTCT  
||||| |||||  
GTCT TGGT CGAAGAGA  
TAA AAG  
CAGACTCATC CTTCT  
||||| |||||  
GTTTGAGTAG GGGGA  
A  
CAA C  
CAGACTCAT GCTT TCT  
||||| |||||

GAM23	<u>469</u>	INHBA	3'	AGAAAGCCATGAGTTTG	59	GTTTGAGTA    TGGA AGA A CAA    C CAGACTCAT    GCTT TCT                GTTTGAGTA    CGAA AGA
GAM23	<u>469</u>	KIF3B	3'	AGAGAAGCTCATAAGTGTG	87	C G    C    CA CA ACT AT AGCTTCTCT                 GT TGA TA TCGAAGAGA G    A    C ACT T A
GAM23	<u>469</u>	MSN	3'	AGAGAAGCCTGTGCCCTG	262	CAG CA CA GCTTCTCT               GTC GT GT CGAAGAGA CC    C AC    CAA
GAM23	<u>469</u>	MTR	3'	AGAGAAGTGTGACCCTG	36	CAG TCAT GCTTCTCT               GTC AGTG TGAAGAGA CC    C ACTC A
GAM23	<u>469</u>	PCDHB9	3'	AGAGAAGTTAGATCCTG	169	CAG ATC AGCTTCTCT               GTC TAG TTGAAGAGA C    A TCATC
GAM23	<u>469</u>	SMARCA3	3'	AGAGAAGCTTCATGTTTG	246	CAGAC AAGCTTCTCT             GTTTG TTCGAAGAGA TAC TCATC
GAM23	<u>469</u>	SMARCA3	3'	AGAGAAGCTTCATGTTTG	66	CAGAC AAGCTTCTCT             GTTTG TTCGAAGAGA TAC TCATC
GAM23	<u>470</u>	SMG1	3'	AGACAGTAGATGAGTCTG	138	CAGACTCATC GCT TCT             GTCTGAGTAG TGA AGA A    C AAG    C
GAM23	<u>469</u>	SNCAIP	5'	AGAAAGGGGGTGAGTCTG	399	CAGACTCATC CTT TCT             GTCTGAGTGG GAA AGA GG A    AA
GAM23	<u>469</u>	SYNGR1	3'	AGGGGAGCGATGAGCTG	86	CAG CTCATC GCTTCTCT                 GTC GAGTAG CGAGGGGA -    -
GAM23	<u>474</u>	UCP2	5'	AGAGAAGCTTGATCTTGGAG	68	CTC ATCAAGCTTCTCT           GAG TAGTTCGAAGAGA GTTC
GAM23	<u>470</u>	BMF	3'	AGAGGCTGATGTGTCTG	229	T    A CAGAC CATCA GCTTCT                   GTCTG GTAGT CGGAGA T
GAM23	<u>472</u>	BNIP2	3'	AGAGAATGTGATGAGTT	278	GACTCATCA TTCTCT             TTGAGTAGT AAGAGA GT C AT
GAM23	<u>472</u>	DDX33	3'	AGAGAAGCCTTGAATC	171	GA TC CAAG CTTCTCT                   CT AG GTTC GAAGAGA

GAM23	<u>475</u>	EML4	3'	AGAAACTTTGGATGAGTT	168	A — C GACTCATC — AAG TTCT               TTGAGTAG TTC AAGA GT A CAAG AGACTCAT CTCTCT             TCTGGGTA GAAGAGA
GAM23	<u>471</u>	EPB41L4	3'	AGAGAAGAAATGGGTCT	187	AA— A CA AA CAG CT TC GCTTCTCT                  GTC GG AG CGAAGAGA C CA A— A T T A— AG C CA CA GCTTCTCT                   TC G GT GT CGAAGAGA
GAM23	<u>469</u>	FLJ11588	5'	AGAGAAGCAGAACGGCCTG	199	— — C A — G T CAG CTCATCAA C TCT                   GTC GAGTAGTT G AGA G — T A — G T CAG CTCATCAA C TCT                   GTC GAGTAGTT G AGA G — T C — TCAA CAGA TCA GCTTCTCT                GTCT GGT CGAAGAGA AC TGA— CA A GACT TC AGCTTCTCT               CTGA AG TCGAAGAGA A AC CA CAG TCAT AGCTTCTCT               GTC AGTG TTGAAGAGA C— TCAA CAGACTCA GCT TCTCT                 GTCTGAGT CGA AGAGA CCAA C CAA AGACT AT GCTTCTCT               TCTGA TA CGAAGAGA C CAA AGACT AT GCTTCTCT               TCTGA TA CGAAGAGA C CAA AGACT AT GCTTCTCT               TCTGA TA CGAAGAGA C A AA— AG CTCATC GCTTCTCT                TC GGGTGG CGAAGAGA — ATC
GAM23	<u>470</u>	FLJ20507	3'	AGATGTTGATGAGGCTG	154	
GAM23	<u>470</u>	FLJ20507	3'	AGATGTTGATGAGGCTG	261	
GAM23	<u>469</u>	FLJ20972	3'	AGAGAAGCAGTTGGCATCTG	205	
GAM23	<u>472</u>	FLJ22233	3'	AGAGAAGCTAGAAAGTC	204	
GAM23	<u>469</u>	FLJ23191	3'	AGAGAAGTTGTGACCTG	198	
GAM23	<u>469</u>	FLJ23468	5'	AGAGAAACCAGCTGAGTCTG	200	
GAM23	<u>471</u>	GIT2	3'	AGAGAAGCATCAGTCT	133	
GAM23	<u>471</u>	GIT2	3'	AGAGAAGCATCAGTCT	231	
GAM23	<u>471</u>	GIT2	3'	AGAGAAGCATCAGTCT	232	
GAM23	<u>471</u>	GRID1	3'	AGAGAAGCCTAGGTGGGCT	285	

GAM23	<u>473</u>	GT650	3'	AAGCTTTCTATGAGTTTG	230	C CAGACTCAT AAGCTT       GTTTGAGTA TTCGAA
GAM23	<u>470</u>	IKKE	3'	AGGACTGTGAGTCTG	124	TCT CA C CAGACTCAT AG TTCT       GTCTGAGTG TC AGGA
GAM23	<u>472</u>	KIAA0254	5'	AGAGGACCGCATGAGTC	131	AA GACTCATC GC TTCTCT       CTGAGTAG CG AGGAGA
GAM23	<u>469</u>	KIAA1026	3'	AGAGAAGCTGCCTCAGTCTG	292	CC CATCA CAGACT AGCTTCTCT       GTCTGA TCGAAGAGA
GAM23	<u>472</u>	KIAA1163	3'	AGAGAAGCATGTCTGAGTT	331	CTCCG T A GACTCA CA GCTTCTCT       TTGAGT GT CGAAGAGA
GAM23	<u>470</u>	KIAA1598	3'	AGAAGCTTCTGTTTGGGCTG	161	CT A TC CAGACTCA AAGCTTCT       GTCTGGGT TTCGAAGA
GAM23	<u>470</u>	KIAA1853	3'	AGAAGCAATGGGCTCTG	287	TTTGTC CAA CAGACTCAT GCTTCT       GTCTGGGTA CGAAGA
GAM23	<u>472</u>	LOXL4	3'	AGAGAAGCTGGTGGATC	213	A CT A GA CATCA GCTTCTCT          CT GTGGT CGAAGAGA
GAM23	<u>469</u>	METAP1	3'	AGAGAAGCGTGAAGTTTG	298	AG CA A CAGACT TCA GCTTCTCT       GTTTGA AGT CGAAGAGA
GAM23	<u>472</u>	MGC11034	3'	AGAGAAGCTCTTTGAAGTT	211	G TCA GACT CA AGCTTCTCT       TTGA GT TCGAAGAGA
GAM23	<u>470</u>	MGC14128	3'	AGAAGCTTTGAGAGCCTG	222	A TTC A A CAG CTC TCAA GCTTCT               GTC GAG AGTT CGAAGA
GAM23	<u>470</u>	MGC16175	5'	AGAGGCTGTGAGTCTG	219	C T CA CAGACTCAT AGCTTCT       GTCTGAGTG TCGGAGA
GAM23	<u>472</u>	MGC2752	5'	AGAGAAGCTCAGTAGAATC	327	C CA GA TC AT AGCTTCTCT              CT AG TG TCGAAGAGA
GAM23	<u>469</u>	MGC34923	3'	AGAGAAGTAGGAAGAGCCTG	254	A A AC A A AA CAG CTC TC GCTTCTCT                   GTC GAG AG TGAAGAGA
GAM23	<u>469</u>	NR1I3	5'	AGAGAAGCAGGAGTCTG	89	C A GA ATCAA

GAM23 469 NYD-SP15 3' AGAGAAGAAATATTTGAGTCTG 208

GAM23 469 OSBPL8 5' AGAGAAGTTGGGGTCTG 177

GAM23 469 PLEKHA4 5' AGAGACCCTGTGAGTCTG 178

GAM23 469 PRKWNK2 3' AGAGATGATTGAGTCTG 372

GAM23 469 PSMD4 3' AGGGTAGCTGAGTCTG 63

GAM23 469 RIS1 3' AGAGAAGCTCTTTGTATCTG 337

GAM23 469 RNF24 3' AGAGGAGTGGATGAGCCTG 114

GAM23 469 SNURF 3' AGAAAAGCGGGTTTTGGGTCTG 96

GAM23 469 SULT4A1 3' AGAGAAGCTTGTGTTTTTG 284

GAM23 469 SV2B 3' AGAGAATTGTGTGAGTCTG 135

GAM23 469 SZF1 5' AGAGAAGCCTAGATATCTG 147

GAM23 469 TLR10 5' AGAGAGGGTATTGAGTCTG 210

GAM23 472 ZNF185 3' AGAGGAGCTTGTGAATC 111

GAM23 470 LOC113612 3' AGAAGGATGAGTTTG 300

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CAGACTC      GCTTCTCT
|||||      |||||
GTCTGAG      CGAAGAGA
      GA
      TCAAG
CAGACTCA      CTTCTCT
|||||      |||||
GTCTGAGT      GAAGAGA
      TTATAAA
      ATCAA
CAGACTC      GCTTCTCT
|||||      |||||
GTCTGGG      TGAAGAGA
      GT
      CA CT
CAGACTCAT AG TCTCT
||||| || |||||
GTCTGAGTG TC AGAGA
      CC
      AGCT
CAGACTCA TCA TCTCT
||||| || |||||
GTCTGAGT AGT AGAGA
      T
      TCAA T
CAGACTCA      GCT CTCT
|||||      |||||
GTCTGAGT      CGA GGGA
      T
      CT TCA
CAGA CA AGCTTCTCT
|||| || |||||
GTCT GT TCGAAGAGA
      AT TTC
      A AA
CAG CTCATC GCTTCTCT
||| ||||| |||||
GTC GAGTAG TGAGGAGA
      C G
      TCAA C
CAGACTCA      GCTT TCT
|||||      |||||
GTCTGGGT      CGAA AGA
      TTTGGG A
      CT T
CAGA CA CAAGCTTCTCT
|||| || |||||
GTTT GT GTTCGAAGAGA
      TT
      GC
CAGACTCAT CAA TTCTCT
||||| || |||||
GTCTGAGTG GTT AAGAGA
      T
      CTC AA
CAGA ATC GCTTCTCT
|||| || |||||
GTCT TAG CGAAGAGA
      A ATC
      TCAAG
CAGACTCA      CTTCTCT
|||||      |||||
GTCTGAGT      GGAGAGA
      TATG
      C T
GA TCA CAAGCTTCTCT
|| || |||||
CT AGT GTTCGAGGAGA
      A
      AAG
CAGACTCATC CTTCT

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GAM23 472 LOC133539 3' AGAGAAGCCCAGGATGGTC 312

GAM23 469 LOC139221 5' AGAGAAGCACATGACCTG 313

GAM23 473 LOC142941 3' AAGTTTATTGTAATGAGTCTG 345

GAM23 469 LOC145717 5' AGAGAGTGGGGGTGAGTCTG 279

GAM23 469 LOC147229 3' AGAGAAGCTGGCAAGAGCTG 325

GAM23 472 LOC147658 3' AGAAAAGTTTGAAGTC 326

GAM23 471 LOC147920 3' AGAGAAGCCTGAGGAATTT 328

GAM23 469 LOC148894 5' AGAGAAGCTCCGTGGGCCTG 347

GAM23 469 LOC150606 3' AGAGAAGCTGGGTGATCTG 349

GAM23 472 LOC150606 3' AGAGAAGCTTGTGGTC 350

GAM23 471 LOC152220 3' AGAGTATTTCTTGATGAATTT 351

GAM23 469 LOC155382 3' AGAGAAGCTGCAGGAGCTG 356

GAM23 471 LOC157621 3' AGAGGGCGAAATGAGTCT 358

GAM23 469 LOC161528 5' AGAGAGTGGGGGTGAGTCTG 342

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|||||
GTTTGAGTAG  GAAGA

      T  AA
GAC CATC  GCTTCTCT
||| |||  |||
CTG GTAG  CGAAGAGA

      GACC
      AC  CAA
CAG TCAT  GCTTCTCT
||| |||  |||
GTC AGTA  CGAAGAGA

      C_  CA_
CAGACTCAT  CAA  GCTT
||| |||  |||
GTCTGAGTA  GTT  TGAA

      AT  ATT
      AA_  T
CAGACTCATC  GCT CTCT
||| |||  |||
GTCTGAGTGG  TGA GAGA

      GGG  -
      A  ATCA_
CAG CTC  AGCTTCTCT
||| |||  |||
GTC GAG  TCGAAGAGA

      AACGG
      CA  C
GACT TCAAGCTT TCT
||| |||  |||
CTGA AGTTTGAA AGA

      A
      C  A  A
AGA TC TCA GCTTCTCT
||| |||  |||
TTT AG AGT CGAAGAGA

      A  G  C
      A  CA
CAG CTCAT  AGCTTCTCT
||| |||  |||
GTC GGGTG  TCGAAGAGA

      C  CC
      C  A
CAGA TCATC AGCTTCTCT
||| |||  |||
GTCT AGTGG TCGAAGAGA

      G
      T  T
GAC CA CAAGCTTCTCT
||| |||  |||
CTG GT GTTCGAAGAGA

      C  -  CTT_
AGA TCATCAAG  CTCT
||| |||  |||
TTT AGTAGTTC  GAGA

      A  TTTAT
      A  ATCA
CAG CTC  AGCTTCTCT
||| |||  |||
GTC GAG  TCGAAGAGA

      GACG
      CAA  T
AGACTCAT  GCT CTCT
||| |||  |||
TCTGAGTA  CGG GAGA

      AAG
      AA_  T
CAGACTCATC  GCT CTCT
||| |||  |||

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-27-

GAM23	<u>469</u>	LOC254249	5'	AGAGAAGTTTGTAATTTG	397	ACG_— CTCAT CAGA CAAGCTTCTCT             GTTT GTTTGAAGAGA
GAM23	<u>469</u>	LOC255475	5'	AGAGAAGCCGAGCTCTG	403	AAAT_— — ATCAA CAGA CTC GCTTCTCT             GTCT GAG CGAAGAGA
GAM23	<u>476</u>	LOC51026	3'	AGAACCCTTGATGAGACT	146	C C_— A C_— AG CTCATCAAG TTCT          TC GAGTAGTTC AAGA
GAM23	<u>470</u>	LOC91308	5'	AGAAGAGATGAGTTTG	274	A CC AAG CAGACTCATC CTTCT       GTTTGAGTAG GAAGA
GAM24	<u>523</u>	CASP10	3'	ATACAACCTGATGTCATATTCC ATTTTGGA	223, 524	A_— C C_— A III TG GA AC CAG TTGTA T                AC CT TG GTC AACAT A
GAM24	<u>523</u>	CASP10	3'	ATACAACCTGATGTCATATTCC ATTTTGGA	224, 524	TATAC TA C III C_— C_— A III TG GA AC CAG TTGTA T                AC CT TG GTC AACAT A
GAM24	<u>477</u>	CHRN3	5'	TTGGGTTCCACTTCGGA	49	TATAC TA C III A A C TCC AA TG GAACCCAG                AGG TT AC CTTGGGTT
GAM24	<u>478</u>	LANCL1	3'	TACAATCTGGACTTGGTA	100	C C_— G C_— TGC AA CCAGATTGTA             ATG TT GGTCTAACAT
GAM24	<u>479</u>	MS4A3	3'	ACATCTGGGTTCAAATTCTG	101	G CA A GC T CA AAT GAACCCAGAT GT             GT TTA CTTGGGTCTA CA
GAM24	<u>480</u>	SLC1A4	3'	TACAATTGTCCCAGTTCCGCAT	64	C AA CCA_— ATGCGAAC GATTGTA             TACGCTTG TTAACAT
GAM24	<u>25</u>	ALLC	5'	TACAAGGATTTCGCATTCTGGG	162	ACCCTG A C_— AGA TCCA AATGCGAA CC TTGTA             GGGT TTACGCTT GG AACAT
GAM24	<u>477</u>	APOL6	3'	CTGGGTTACATTTTGGA	206	C TA_— C TCCAAAATG GAACCCAG             AGGTTTAC CTTGGGTC
GAM24	<u>477</u>	CBX6	3'	TTGGGCTCCATTCTGGA	128	A C A TCCA AATG GA CCCAG             AGGT TTAC CT GGGTT
GAM24	<u>477</u>	FLJ10055	3'	TTGGGAGTCCCATTTTGGA	156	C C_— C A_— TCCAAAATG GA CCCAG             AGGTTTAC CT GGGTT



GAM24	<u>481</u>	FLJ22059	5'	CAGTCTGGACCAGCACCTTGGA	191	AA GAAC TCCAA TGC CCAGATTG                 AGGTT ACG GGTCTGAC CC ACCA A C TCCA AATG GAACCCAG                 AGGT TTAC CTTGGGTT C A A TCCAAAATGCG ACCCAG                 AGGTTTACGT TGGGTT C C CCCAG TCCAAAATG GAA ATTGT                 AGGTTTAC CTT TGACA A - C GA AAAATGCGAAC CA TTGT                 TTTACGTTTG GT AACA A AACCCA CAAAATGCG GATTGT                 GTTTACGC TTAACA C AACC GA CAAAATGCG CA TTGTA                 GTTTACGC GT GACAT ATTA A C C TT TCCAAAATG GAACC AGA GTA                 AGGTTTAC CTTGG TCT CAT A T T C TCCAAAATGC GAA CC                 AGGTTTACG CTT GG A AA AAAT AACC TCCA GCG CAGATTGT                 GGGT TGC GTCTAACA C AA GTTAGA A TCTCTG CC GATCTGAG                 GGAGAC GG CTAGACTC AG AC CCAGA TCTGGTTAGA TCT GAGC                 AGACCAATCT AGA CTCG A T AC A TCTGGTTAG CAG TCTGAGC                 AGACCAATT GTT AGACTCG G AGAC A TCTCTGGTT CAG TCTGAG                 AGAGACTAA GTC AGACTC C AGACCAGA A
GAM24	<u>477</u>	KCNH8	3'	TTGGGTTCACATTCTGGA	252	
GAM24	<u>477</u>	KIAA0870	3'	TTGGGTCTGCATTTTGGA	339	
GAM24	<u>482</u>	KIAA1157	3'	ACAGTATTCCATTTTGGA	296	
GAM24	<u>483</u>	PRO1048	3'	ACAATGAGTTTGCATTTT	163	
GAM24	<u>479</u>	PRO1787	3'	ACAATCCGCATTTTG	165	
GAM24	<u>484</u>	UBE2G1	3'	TACAGATGATTACGCATTTTG	67	
GAM24	<u>25</u>	LOC122402	3'	TACTTCTTGGTTCACATTTTGG A	306	
GAM24	<u>485</u>	LOC153592	3'	GGAATTCAGCATTTTGGA	355	
GAM24	<u>482</u>	LOC256158	5'	ACAATCTGAACGTCTGGG	404	
GAM25	<u>486</u>	ITGA5	3'	CTCAGATCCAGGGACAGAGG	264	
GAM25	<u>487</u>	SF3B3	3'	GCTCTAGAATCTAACCAGA	116	
GAM25	<u>487</u>	SLC4A4	3'	GCTCAGAGTTGTTAACCAGA	71	
GAM25	<u>486</u>	ZNF180	3'	CTCAGACCTGAATCAGAGA	120	
GAM25	<u>487</u>	AP1G2	5'	GCCCAGGCACGCCGACCAGAG	233	

A

GAM25	<u>488</u>	BCL2L1	3'	GCCCAGATCTGGTCCCTTGCAG	241
GAM25	<u>486</u>	FLJ25012	5'	CTCAGATCTGAAAAGCACAAGA	250
GAM25	<u>489</u>	FLJ31952	3'	CAAATCTGGTTCTGAAAG	253
GAM25	<u>490</u>	MDS025	3'	CTCAGACCTGGTTTGAGATAGA	184
GAM25	<u>487</u>	MGC32043	3'	GCTCAGATCTGATGCTTCAAGA	249
GAM25	<u>486</u>	MSI2	3'	CTCCCCATCCCAACCAGAGA	245
GAM25	<u>487</u>	ZNF271	5'	GCTCAGATCTGGTTAAACATCA	395
				GAGA	
GAM25	<u>487</u>	LOC144508	5'	GCTCAGATCCATGTGCCAGGGA	362
GAM25	<u>486</u>	LOC145845	3'	CTCAAATCCCACCAGAGA	346
GAM26	<u>491</u>	CDH19	3'	GAAAATTTAAAGGAGCAA	182
GAM26	<u>492</u>	CRYGS	5'	TGGGAAAACCACTCTATGCACC	152
				AA	
GAM26	<u>493</u>	CYP1B1	3'	GAAAATTGAAAAGTACAATAA	33
GAM26	<u>494</u>	GLI3	3'	GGAAAAAAGACTGCAACCAA	35
GAM26	<u>493</u>	PCLO	3'	GAAGATAATGCAACCAA	391

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TCTCTGGTT      TCTG GC
|||||
AGAGACCAG      GGAC CG
      CCGGCAC_ C
      GTTA_ A
CTG      GACCAGATCTG GC
|||      |||||
GAC      CTGGTCTAGAC CG
      GTTCC C
      C_ AGAC
TCT TG GTT      CAGATCTGAG
||| ||| |||      |||||
AGA AC CGA      GTCTAGACTC
      A AAA_ C
      GG_ C
CT TTAGA CCAGAT TG
|| ||||| ||||| |||
GA AGTCT GGTCTA AC
      A_ T_ A
      G_ A
TCTG TTAGACCAG TCTGAG
|||| ||||| |||||
AGAT AGTTTGCTC AGACTC
      AG C
      GGTT AC_
TCT AG CAGATCTGAGC
||| ||| |||||
AGA TC GTCTAGACTCG
      ACT_ GTA
      AGACCA CT_
TCTCTGGTT      GAT GAG
|||||
AGAGACCAA      CTA CTC
      CC_ CCC
      A
TCTCTG GTT GACCAGATCTGAGC
||||| ||| |||||
AGAGAC CAA TTGGTCTAGACTCG
      TA A
      TAGACCA
TCTCTGGT      GATCTGAGC
|||||
AGGGACCG      CTAGACTCG
      TGTAC_
      TAGACCA C
TCTCTGGT      GAT TGAG
|||||
AGAGACCA      CTA ACTC
      CC_ A
      A_
TTGC CTTTAAATTTTC
||| |||||
AACG GAAATTTAAAG
      AG
      T CTTTAA_
TTGGT GCA      TTTTCCCA
||||| ||| |||||
AACCA CGT      AAAAGGT
      ATCTGACC
      C A_
TTGGTTG ACTTT AATTTTC
||||| ||||| |||||
AATCAAC TGAAA TTAAAAG
      A AG
      C AAA
TTGGTTGCA TTT TTTTCC
||||| ||| |||||
AACCAACGT AGA AAAAGG
      C AA_
      CTTTAA
TTGGTTGCA      ATTTTTC

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GAM26 492 PPP2R5A 3' TGGGAAAGTAAACCAA 102

GAM26 492 PTER 3' TGAGAAAATTTAAAGTGTCT 207  
AG

GAM26 495 RFX5 3' GGGAAAAGCAGTAAACCAA 39

GAM26 494 CSMD1 3' GGAGTATTAAAGTGAACCAA 301

GAM26 493 MGC15438 3' GAAAGAAAGCGCAGCCAA 220

GAM26 494 NYD-SP18 3' GGAGAAAAGTGAACCAA 217

GAM26 494 OLFM3 3' GGAAAAATAATGTAACCAA 340

GAM26 495 RPL13A 3' GGGAAGATGCACAACCAA 115

GAM26 496 LOC129452 3' AGAATGGACAAGCGCAACCAA 310

GAM26 494 LOC150197 3' GGATTAAAGTGAACCAA 335

GAM26 494 LOC162239 3' GGAAATTATAAATGGCAACCAA 344

GAM26 496 LOC219972 3' GAAATGGCAAGTGAACCAA 379

GAM27 497 DDX6 3' ATTGTGACAAGAATTGTTACC 80

GAM27 498 LOC126917 3' GCAGTGGGTCTGTTGCCA 309

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AACCAACGT
AA
GC TAAATTT
TTGGTT ACTT TCCCA
|||||
AACCAA TGAA AGGGT
A
TT C
TTGG GCACCTTTAAATTTTTC CA
|||||
GATC TGTGAAATTTAAAG GT
TT A
GC TTAAA
TTGGTT ACT TTTTCCC
|||||
AACCAA TGA AAAAGGG
A CG
G ATT
TTGGTT CACTTTAA TTCC
|||||
AACCAA GTGAAATT GAGG
G AT
A AAA
TTGGTTGC CTTT TTTTC
|||||
AACCGACG GAAA GAAAG
C
C AAAT
TTGGTTGCA TTT TTTCC
|||||
AACCAACGT AAA AGAGG
C
C TAAA
TTGGTTGCA TT TTTTCC
|||||
AACCAATGT AA AAAAGG
TA
CACTTTTAA
TTGGTTG CTTT TTTTCCC
|||||
AACCAAC TAGAAGGG
ACG
A TAA
TTGGTTGC CTT ATTTT
|||||
AACCAACG GAA TAAGA
C CAGG
G ATTT
TTGGTT CACTTTAA TCC
|||||
AACCAA GTGAAATT AGG
G
AC AAT
TTGGTTGC TTTA TTTCC
|||||
AACCAACG AAAT AAAGG
GT ATT
TAA
TTGGTTGCACTT ATTTT
|||||
AACCAACGTGAA TAAAG
CGG
C CCC C
GG AACGA CT GTCACAAT
|||
CC TTGTT GA CAGTGTTA
A AA A
TGGCAAC GACCC CT GT
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GAM27	<u>499</u>	LOC170395	3'	TATTGTTTCTGGGTGTGCCA	316
GAM28	<u>500</u>	ABCC3	3'	TGCCCCCTGGCTGTGCTCTAC	170
GAM28	<u>500</u>	CASP3	3'	TGCCCCCTGGATCTACCAGCAT	225
GAM28	<u>500</u>	CASP3	3'	TGCCCCCTGGATCTACCAGCAT	79
GAM28	<u>501</u>	EMS1	3'	CCCTGGATCCTCACACTA	90
GAM28	<u>501</u>	EMS1	3'	CCCTGGATCCTCACACTA	240
GAM28	<u>500</u>	MLLT2	3'	TGCCCCCTGGACATGTTTCTCTAC	97
GAM28	<u>502</u>	TACC1	3'	TGCCCCCAGATGTTCTGGGCT	104
GAM28	<u>503</u>	TNFSF6	3'	CCAGGTGTTCTACACTCA	42
GAM28	<u>504</u>	UBB	3'	TGGCATTACTCTGCACTATA	166
GAM28	<u>505</u>	AKAP10	3'	TGCCCCCTTTGGAATTCTGCACT	113
GAM28	<u>506</u>	DECR2	3'	GCCCCCTCTGTCTCTGCAC	176
GAM28	<u>507</u>	KIAA0240	3'	GCCCCCTGTGTCCCACTA	383
GAM28	<u>506</u>	MGC16385	5'	GCCCCCTGGACGTTTCTGCCGC	255

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ACCGTTG CTGGG GA CG
      T      T
      G      CTCGTC
TGGCAAC ACCC      ACAATA
||||| ||| ||| |||
ACCGTTG TGGG      TGTAT
      TCTT
      C A T
GTG AG ACA CCAGGGGCA
||| || ||| ||| ||| |||
CAT TC TGT GGTCCCCGT
      C G C
      AGAAC
GTGC      ATCCAGGGGCA
|||| ||| ||| ||| |||
TACG      TAGGTCCCCGT
      ACCATC
      AGAAC
GTGC      ATCCAGGGGCA
|||| ||| ||| ||| |||
TACG      TAGGTCCCCGT
      ACCATC
      CA AC
TAGTG GA ATCCAGGG
|||| || ||| ||| |||
ATCAC CT TAGGTCCC
      A CC
      CA AC
TAGTG GA ATCCAGGG
|||| || ||| ||| |||
ATCAC CT TAGGTCCC
      A CC
      CA
GTG GAACA TCCAGGGGCA
||| ||| ||| ||| |||
CAT TTTGT AGGTCCCCGT
      CC AC
      G CA
TAGT CAG AACATC GGGGCA
|||| ||| ||| ||| |||
GTCG GTC TTGTAG CCCCCT
      G C AC
      T C CA
A AGTG AGAACATC GG
| ||| ||| ||| ||| |||
A TCAC TCTGTGG CC
      C A A
      AC
TATAGTGCAGA AT CCA
|||| ||| ||| ||| |||
ATATCACGTCT TA GGT
      CAT C
      CA
AGTGCAGAA TCCA GGGGCA
|||| ||| ||| ||| |||
TCACGTCTT AGGT CCCCCT
      A TT
      TCC
GTGCAGA ACA AGGGGC
|||| ||| ||| ||| |||
CACGTCT TGT TCCCCG
      C C
      CA A TC
TAGTG GA CA CAGGGGC
|||| || ||| ||| |||
ATCAC CT GT GTCCCCG
      C A
      GTG CAGAA C TCCAGGGGC
||| ||| ||| ||| |||
CGC GTCTT G AGGTCCCCG

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GAM28	<u>508</u>	MGC5139	5'	GCCCCCTGGGCACACTGTA	305	C T C CAGAACA TATAGTG TCCAGGGGC             ATGTCAC GGGTCCCCG
GAM28	<u>509</u>	P5-1	3'	CCCCTGGATGCCCTAACCCT	110	AC C AA AGTG AG CATCCAGGGG              TCAC TC GTAGTCCCC
GAM28	<u>510</u>	TED	3'	CCCCTGGGCCCTGCCTA	143	CAA CCC T AACA TAG GCAG TCCAGGGG               ATC CGTC GGGTCCCC
GAM28	<u>502</u>	LOC133418	3'	TGCTCTAAAGCTCTGCACTA	311	CC ACATCCA TAGTGCAGA GGGGCA             ATCACGTCT TCTCGT
GAM28	<u>511</u>	LOC152402	3'	GCCCTTACATTCTGCACT	353	CGAAA CATCC AGTGCAGAA AGGGGC             TCACGTCTT TTCCCG
GAM28	<u>512</u>	LOC158677	3'	TGCCCCCTGGATATCAGCAATAT	360	A G A AC TATA TGC GA ATCCAGGGGCA                   ATAT ACG CT TAGGTCCCCGT
GAM28	<u>501</u>	LOC221715	3'	CCACTGTGCTTGCCTA	390	A A A AA TC TAGTGCAG CA CAG GG              ATCACGTT GT GTC CC
GAM28	<u>504</u>	LOC254746	3'	TGGCATTACTCTGCACTATA	394	C AC A TATAGTGCAGA AT CCA              ATATCACGTCT TA GGT
GAM28	<u>502</u>	LOC255098	3'	TGCTCTAAAGCTCTGCACTA	396	CAT C ACATCCA TAGTGCAGA GGGGCA             ATCACGTCT TCTCGT
GAM29	<u>513</u>	ADAM19	3'	CTGATGGAGATGCTCAAGGC	228	CGAAA AG TATGG GCCTT GCATCTCC CAG                CGGAA CGTAGAGG GTC
GAM29	<u>514</u>	LFG	3'	TGCCACAGGCCTAAGGCT	319	CT TA ATCTC A AGCCTTAGGC CT TGGCA                TCGGAATCCG GA ACCGT
GAM29	<u>515</u>	NOLA2	5'	GGAAGTGATGCCTAAAGCT	393	C AGC TTAGGCATC TCC               TCG AATCCGTAG AGG
GAM29	<u>514</u>	FLJ10751	3'	CCAGAGACACCTGAGGC	158	A TGA CA CTA GCCTTAGG TCTC TGG               CGGAGTCC AGAG ACC
GAM29	<u>514</u>	FLJ10751	3'	CCAGAGACACCTGAGGC	159	AC CTA CA GCCTTAGG TCTC TGG               CGGAGTCC AGAG ACC AC

GAM29 513 FLJ10925 5' CTGCCCCAGGGACACCTAAGG 160  
C

GAM29 517 KIAA1118 3' GTGGTTGAGATGCCACGGCT 289

GAM29 518 KIAA1649 3' CTGCCATTCTGTGCCTAGGCT 215

GAM29 513 LIMR 3' CTGCCATCTGCTGCCTAGGC 157

GAM29 516 MGC14161 5' CCAGAGAGATGCCAAAGGC 221

GAM29 519 NJMU-R1 3' CATGAAGAAATGCCTGAAGC 188

GAM29 518 SEMA3E 3' CTGTTGTGAGAAATGCCAGGC 119  
T

GAM29 520 YKT6 3' CTGCCATAGATACCCTAAG 106

GAM29 521 LOC142972 5' GCCACAGGAGATGCCCAAAGC 271

GAM29 514 LOC143689 3' TGCCATAAGCTCAAGGCT 318

GAM29 522 LOC148930 5' CCATAGGGAGCCTAAG 332

GAM29 516 LOC220469 3' CCAAGGGATGCCCAAAGC 317

GAM29 519 LOC253782 3' CATAAGAGCACCTAAGGC 398

GAM29 514 LOC92078 5' TGCCCAGAGGCCTAAGGCT 282

CA T AT\_

GCCTTAGG TC CCT GGCAG  
||||| ||| |||  
CGGAATCC AG GGA CCGTC  
AC - CCC

TTA CT G

AGCC GGCATCTC AT GC  
||||| ||| |||  
TCGG CCGTAGAG TG TG

CAC T G

T CTCCT

AGCCT AGGCAT ATGGCAG  
||||| ||| |||  
TCGGA TCCGTG TACCGTC

TCTT\_

T- TCTCCT

GCCT AGGCA ATGGCAG  
||||| ||| |||  
CGGA TCCGT TACCGTC

CGTC\_

-A CTA

GCCTT GGCATCTC TGG  
||||| ||| |||  
CGGAA CCGTAGAG ACC

A AG\_

C C C\_

GC TTAGGCAT TC TATG  
|| ||| ||| |||  
CG AGTCCGTA AG GTAC

A A AA

TA C C TG

AGCCT GGCAT TC TA GCAG  
||||| ||| ||| |||  
TCGGA CCGTA AG GT TGTC

C\_ A A GT

CATCTC

CTTAGG CTATGGCAG  
||||| ||| ||| |||  
GAATCC GATACCGTC

CATA\_

C A A

GC TT GGCATCTCCT TGGC  
|| || ||| ||| ||| |||  
CG AA CCGTAGAGGA ACCG

A C C

AG ATCTCC

AGCCTT GC TATGGCA  
||||| ||| ||| |||  
TCGGAA CG ATACCGT

CT A\_

A T

CTTAGGC TC CCTATGG  
||||| ||| ||| |||  
GAATCCG AG GGATACC

C A - - T A

GC TT GGCATC CCT TGG  
|| || ||| ||| ||| |||  
CG AA CCGTAG GGA ACC

A C

CAT - C -

GCCTTAGG CTC TATG  
||||| ||| ||| |||  
CGGAATCC GAG ATAC

AC\_ A

A CCTAT

AGCCTTAGGC TCT GGCA  
||||| ||| ||| |||  
TCGGAATCCG AGA CCGT